

(iii)

Blast Result



Blast 2 Sequences results

PubMed

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BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

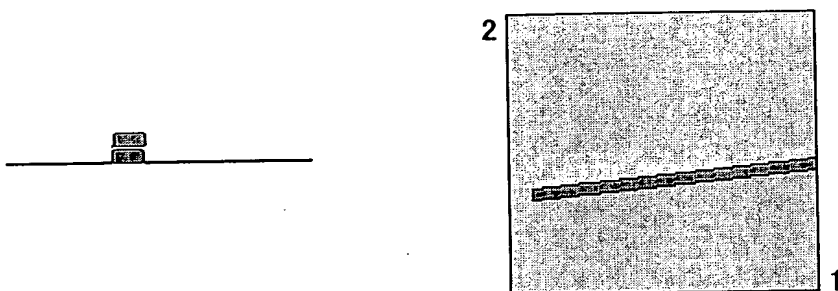
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1

Length = 459 (1 .. 459)

Sequence 2: lcl|2_seq_2

Length = 4258 (1 .. 4258)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 812 bits (422), Expect = 0.0
 Identities = 422/422 (100%), Gaps = 0/422 (0%)
 Strand=Plus/Plus

Query	38	GGAACATCGAGGACATCTACCGCTGCCAGAAGGCCTTCGTGAAGGCCCTGGAGCAGAGGT	97
Sbjct	1512	GGAACATCGAGGACATCTACCGCTGCCAGAAGGCCTTCGTGAAGGCCCTGGAGCAGAGGT	1571
Query	98	TCAACGCGAGCGCCACACCTGAGCGAGCTGGGTGCCTGCTTCTGGAGCATCAAGCCG	157
Sbjct	1572	TCAACGCGAGCGCCACACCTGAGCGAGCTGGGTGCCTGCTTCTGGAGCATCAAGCCG	1631
Query	158	ACTTCCAGATCTACTCGGAGTACTGCAATAACCAACCCCAACGCCTGCGTGGAGCTCTCCC	217
Sbjct	1632	ACTTCCAGATCTACTCGGAGTACTGCAATAACCAACCCCAACGCCTGCGTGGAGCTCTCCC	1691
Query	218	GGCTACCAAGCTCAGCAAGTACGTACTTCTTCGAGGCCTGCCGGCTGCTGCAGAAGA	277
Sbjct	1692	GGCTACCAAGCTCAGCAAGTACGTACTTCTTCGAGGCCTGCCGGCTGCTGCAGAAGA	1751
Query	278	TGATTGACATCTCCCTGGATGGCTTCTGCTGACTCCGGTGCAGAAGATCTGCAAGTACC	337
Sbjct	1752	TGATTGACATCTCCCTGGATGGCTTCTGCTGACTCCGGTGCAGAAGATCTGCAAGTACC	1811

Blast Result

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Query 338 CTCTGCAGCTGGCCGAGCTGCTCAAATACACGCACCCCCAGCACAGGGACTTCAAGGATG 397
          |||
Sbjct 1812 CTCTGCAGCTGGCCGAGCTGCTCAAATACACGCACCCCCAGCACAGGGACTTCAAGGATG 1871

Query 398 TTGAAGCCGCCTTGCATGCCATGAAGAACGTGGCCCAGCTCATCAACGAGCGGAAGCGGA 457
          |||
Sbjct 1872 TTGAAGCCGCCTTGCATGCCATGAAGAACGTGGCCCAGCTCATCAACGAGCGGAAGCGGA 1931

Query 458 GA 459
          ||
Sbjct 1932 GA 1933

```

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 146
 Number of extensions: 5
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 1
 Number of HSP's successfully gapped: 1
 Length of query: 459
 Length of database: 18,725,440,322
 Length adjustment: 26
 Effective length of query: 433
 Effective length of database: 18,725,440,296
 Effective search space: 8108115648168
 Effective search space used: 8108115648168
 X1: 11 (21.1 bits)
 X2: 26 (50.0 bits)
 X3: 26 (50.0 bits)
 S1: 14 (27.6 bits)
 S2: 21 (41.1 bits)

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